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RAW SEQUENCE LISTING

DATE: 01/27/2003

PATENT APPLICATION: US/09/922,225A

TIME: 15:21:36

Input Set : A:\Ea4672.txt

Output Set: N:\CRF4\01272003\I922225A.raw

4 <110> APPLICANT: Evans, Glen A.
 6 <120> TITLE OF INVENTION: Nucleic Acids and Encoded Polypeptides
 7 Associated with Bipolar Disorder
 10 <130> FILE REFERENCE: P-EA 4672
 12 <140> CURRENT APPLICATION NUMBER: US 09/922,225A
 C--> 13 <141> CURRENT FILING DATE: 2003-01-14
 15 <160> NUMBER OF SEQ ID NOS: 117
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1961
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (10)...(1842)
 28 <400> SEQUENCE: 1
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 30 Met Ala Ser Arg Gly Ala Arg Gln Arg Leu Lys Gly Ser Gly
 31 1 5 10
 33 gcc agc agt ggg gat acg gcc ccg gct gcg gac aag ctg cgg gag ctg 99
 34 Ala Ser Ser Gly Asp Thr Ala Pro Ala Ala Asp Lys Leu Arg Glu Leu
 35 15 20 25 30
 37 ctg ggc agc cga gag gcg ggc ggc gcg gag cac cgg acc gag tta tct 147
 38 Leu Gly Ser Arg Glu Ala Gly Gly Ala Glu His Arg Thr Glu Leu Ser
 39 35 40 45
 41 ggg aac aaa gca gga caa gtc tgg gca cct gaa gga tct act gct ttc 195
 42 Gly Asn Lys Ala Gly Gln Val Trp Ala Pro Glu Gly Ser Thr Ala Phe
 43 50 55 60
 45 aag tgt ctg ctt tca gca agg tta tgt gct gct ctc ctg agc aac atc 243
 46 Lys Cys Leu Leu Ser Ala Arg Leu Cys Ala Ala Leu Leu Ser Asn Ile
 47 65 70 75
 49 tct gac tgt gat gaa aca ttc aac tac tgg gag cca aca cac tac ctc 291
 50 Ser Asp Cys Asp Glu Thr Phe Asn Tyr Trp Glu Pro Thr His Tyr Leu
 51 80 85 90
 53 atc tat ggg gaa ggg ttt cag act tgg gaa tat tcc cca gca tat gcc 339
 54 Ile Tyr Gly Glu Gly Phe Gln Thr Trp Glu Tyr Ser Pro Ala Tyr Ala
 55 95 100 105 110
 57 att cgc tcc tat gct tac ctg ttg ctt cat gcc tgg cca gct gca ttt 387
 58 Ile Arg Ser Tyr Ala Tyr Leu Leu Leu His Ala Trp Pro Ala Ala Phe
 59 115 120 125
 61 cat gca aga att cta caa act aat aag att ctt gtg ttt tac ttt ttg 435
 62 His Ala Arg Ile Leu Gln Thr Asn Lys Ile Leu Val Phe Tyr Phe Leu
 63 130 135 140

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65 cga tgt ctt ctg gct ttt gtg agc tgt att tgt gaa ctt tac ttt tac 483
66 Arg Cys Leu Leu Ala Phe Val Ser Cys Ile Cys Glu Leu Tyr Phe Tyr
67      145      150      155
69 aag gct gtg tgc aag aag ttt ggg ttg cac gtg agt cga atg atg cta 531
70 Lys Ala Val Cys Lys Lys Phe Gly Leu His Val Ser Arg Met Met Leu
71      160      165      170
73 gcc ttc ttg gtt ctc agc act ggc atg ttt tgc tca tca tca gca ttc 579
74 Ala Phe Leu Val Leu Ser Thr Gly Met Phe Cys Ser Ser Ser Ala Phe
75 175      180      185      190
77 ctt cct agt agc ttc tgt atg tac act acg ttg ata gcc atg act gga 627
78 Leu Pro Ser Ser Phe Cys Met Tyr Thr Thr Leu Ile Ala Met Thr Gly
79      195      200      205
81 tgg tat atg gac aag act tcc att gct gtg ctg gga gta gca gct ggg 675
82 Trp Tyr Met Asp Lys Thr Ser Ile Ala Val Leu Gly Val Ala Ala Gly
83      210      215      220
85 gct atc tta ggc tgg cca ttc agt gca gct ctt ggt tta ccc att gcc 723
86 Ala Ile Leu Gly Trp Pro Phe Ser Ala Ala Leu Gly Leu Pro Ile Ala
87      225      230      235
89 ttt gat ttg ctg gtc atg aaa cac agg tgg aag agt ttc ttt cat tgg 771
90 Phe Asp Leu Leu Val Met Lys His Arg Trp Lys Ser Phe Phe His Trp
91      240      245      250
93 tcg ctg atg gcc ctc ata cta ttt ctg gtg cct gtg gtg gtc att gac 819
94 Ser Leu Met Ala Leu Ile Leu Phe Leu Val Pro Val Val Val Ile Asp
95 255      260      265      270
97 agc tac tat tat ggg aag ttg gtg att gca cca ctc aac att gtt ttg 867
98 Ser Tyr Tyr Tyr Gly Lys Leu Val Ile Ala Pro Leu Asn Ile Val Leu
99      275      280      285
101 tat aat gtc ttt act cct cat gga cct gat ctt tat ggt aca gaa ccc 915
102 Tyr Asn Val Phe Thr Pro His Gly Pro Asp Leu Tyr Gly Thr Glu Pro
103      290      295      300
105 tgg tat ttc tat tta att aat gga ttt ctg aat ttc aat gta gcc ttt 963
106 Trp Tyr Phe Tyr Leu Ile Asn Gly Phe Leu Asn Phe Asn Val Ala Phe
107      305      310      315
109 gct ttg gct ctc cta gtc cta cca ctg act tct ctt atg gaa tac ctg 1011
110 Ala Leu Ala Leu Leu Val Leu Pro Leu Thr Ser Leu Met Glu Tyr Leu
111      320      325      330
113 ctg cag aga ttt cat gtt cag aat tta ggc cac ccg tat tgg ctt acc 1059
114 Leu Gln Arg Phe His Val Gln Asn Leu Gly His Pro Tyr Trp Leu Thr
115 335      340      345      350
117 ttg gct cca atg tat att tgg ttt ata att ttc ttc atc cag cct cac 1107
118 Leu Ala Pro Met Tyr Ile Trp Phe Ile Ile Phe Phe Ile Gln Pro His
119      355      360      365
121 aaa gag gag aga ttt ctt ttc cct gtg tat cca ctt ata tgt ctc tgt 1155
122 Lys Glu Glu Arg Phe Leu Phe Pro Val Tyr Pro Leu Ile Cys Leu Cys
123      370      375      380
125 ggc gct gtg gct ctc tct gca ctt cag aaa tgt tac cac ttt gtg ttt 1203
126 Gly Ala Val Ala Leu Ser Ala Leu Gln Lys Cys Tyr His Phe Val Phe
127      385      390      395
129 caa cga tat cgc ctg gag cac tat act gtg aca tcg aat tgg ctg gca 1251

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130 Gln Arg Tyr Arg Leu Glu His Tyr Thr Val Thr Ser Asn Trp Leu Ala
131      400                      405                      410
133 tta gga act gtc ttc ctg ttt ggg ctc ttg tca ttt tct cgc tct gtg 1299
134 Leu Gly Thr Val Phe Leu Phe Gly Leu Leu Ser Phe Ser Arg Ser Val
135 415                      420                      425                      430
137 gca ctg ttc aga gga tat cac ggg ccc ctt gat ttg tat cca gaa ttt 1347
138 Ala Leu Phe Arg Gly Tyr His Gly Pro Leu Asp Leu Tyr Pro Glu Phe
139      435                      440                      445
141 tac cga att gct aca gac cca acc atc cac act gtc cca gaa ggc aga 1395
142 Tyr Arg Ile Ala Thr Asp Pro Thr Ile His Thr Val Pro Glu Gly Arg
143      450                      455                      460
145 cct gtg aat gtc tgt gtg gga aaa gag tgg tat cga ttt ccc agc agc 1443
146 Pro Val Asn Val Cys Val Gly Lys Glu Trp Tyr Arg Phe Pro Ser Ser
147      465                      470                      475
149 ttc ctt ctt cct gac aat tgg cag ctt cag ttc att cca tca gag ttc 1491
150 Phe Leu Leu Pro Asp Asn Trp Gln Leu Gln Phe Ile Pro Ser Glu Phe
151      480                      485                      490
153 aga ggt cag tta cca aaa cct ttt gca gaa gga cct ctg gcc acc cgg 1539
154 Arg Gly Gln Leu Pro Lys Pro Phe Ala Glu Gly Pro Leu Ala Thr Arg
155 495                      500                      505                      510
157 att gtt cct act gac atg aat gac cag aat cta gaa gag cca tcc aga 1587
158 Ile Val Pro Thr Asp Met Asn Asp Gln Asn Leu Glu Glu Pro Ser Arg
159      515                      520                      525
161 tat att gat atc agt aaa tgc cat tat tta gtg gat ttg gac acc atg 1635
162 Tyr Ile Asp Ile Ser Lys Cys His Tyr Leu Val Asp Leu Asp Thr Met
163      530                      535                      540
165 aga gaa aca ccc cgg gag cca aaa tat tca tcc aat aaa gaa gaa tgg 1683
166 Arg Glu Thr Pro Arg Glu Pro Lys Tyr Ser Ser Asn Lys Glu Glu Trp
167      545                      550                      555
169 atc agc ttg gcc tat aga cca ttc ctt gat gct tct aga tct tca aag 1731
170 Ile Ser Leu Ala Tyr Arg Pro Phe Leu Asp Ala Ser Arg Ser Ser Lys
171      560                      565                      570
173 ctg ctg cgg gca ttc tat gtc ccc ttc ctg tca gat cag tat aca gtg 1779
174 Leu Leu Arg Ala Phe Tyr Val Pro Phe Leu Ser Asp Gln Tyr Thr Val
175 575                      580                      585                      590
177 tac gta aac tac acc atc ctc aaa ccc cgg aaa gca aag caa atc agg 1827
178 Tyr Val Asn Tyr Thr Ile Leu Lys Pro Arg Lys Ala Lys Gln Ile Arg
179      595                      600                      605
181 aag aaa agt gga ggt tagcaacaca cctgtggccc caaaggacaa ccatttgtt 1882
182 Lys Lys Ser Gly Gly
183      610
185 aactattgat tccagtgacc tgactccctg caagtcacg cctgtaacat ttgtaataaa 1942
186 ggtcttctga catgaaaaa 1961
188 <210> SEQ ID NO: 2
189 <211> LENGTH: 611
190 <212> TYPE: PRT
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 2
194 Met Ala Ser Arg Gly Ala Arg Gln Arg Leu Lys Gly Ser Gly Ala Ser

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195 1 5 10 15
196 Ser Gly Asp Thr Ala Pro Ala Ala Asp Lys Leu Arg Glu Leu Leu Gly
197 20 25 30
198 Ser Arg Glu Ala Gly Gly Ala Glu His Arg Thr Glu Leu Ser Gly Asn
199 35 40 45
200 Lys Ala Gly Gln Val Trp Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys
201 50 55 60
202 Leu Leu Ser Ala Arg Leu Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp
203 65 70 75 80
204 Cys Asp Glu Thr Phe Asn Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr
205 85 90 95
206 Gly Glu Gly Phe Gln Thr Trp Glu Tyr Ser Pro Ala Tyr Ala Ile Arg
207 100 105 110
208 Ser Tyr Ala Tyr Leu Leu Leu His Ala Trp Pro Ala Ala Phe His Ala
209 115 120 125
210 Arg Ile Leu Gln Thr Asn Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys
211 130 135 140
212 Leu Leu Ala Phe Val Ser Cys Ile Cys Glu Leu Tyr Phe Tyr Lys Ala
213 145 150 155 160
214 Val Cys Lys Lys Phe Gly Leu His Val Ser Arg Met Met Leu Ala Phe
215 165 170 175
216 Leu Val Leu Ser Thr Gly Met Phe Cys Ser Ser Ser Ala Phe Leu Pro
217 180 185 190
218 Ser Ser Phe Cys Met Tyr Thr Thr Leu Ile Ala Met Thr Gly Trp Tyr
219 195 200 205
220 Met Asp Lys Thr Ser Ile Ala Val Leu Gly Val Ala Ala Gly Ala Ile
221 210 215 220
222 Leu Gly Trp Pro Phe Ser Ala Ala Leu Gly Leu Pro Ile Ala Phe Asp
223 225 230 235 240
224 Leu Leu Val Met Lys His Arg Trp Lys Ser Phe Phe His Trp Ser Leu
225 245 250 255
226 Met Ala Leu Ile Leu Phe Leu Val Pro Val Val Val Ile Asp Ser Tyr
227 260 265 270
228 Tyr Tyr Gly Lys Leu Val Ile Ala Pro Leu Asn Ile Val Leu Tyr Asn
229 275 280 285
230 Val Phe Thr Pro His Gly Pro Asp Leu Tyr Gly Thr Glu Pro Trp Tyr
231 290 295 300
232 Phe Tyr Leu Ile Asn Gly Phe Leu Asn Phe Asn Val Ala Phe Ala Leu
233 305 310 315 320
234 Ala Leu Leu Val Leu Pro Leu Thr Ser Leu Met Glu Tyr Leu Leu Gln
235 325 330 335
236 Arg Phe His Val Gln Asn Leu Gly His Pro Tyr Trp Leu Thr Leu Ala
237 340 345 350
238 Pro Met Tyr Ile Trp Phe Ile Ile Phe Phe Ile Gln Pro His Lys Glu
239 355 360 365
240 Glu Arg Phe Leu Phe Pro Val Tyr Pro Leu Ile Cys Leu Cys Gly Ala
241 370 375 380
242 Val Ala Leu Ser Ala Leu Gln Lys Cys Tyr His Phe Val Phe Gln Arg
243 385 390 395 400

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244 Tyr Arg Leu Glu His Tyr Thr Val Thr Ser Asn Trp Leu Ala Leu Gly
245                               405                               410                               415
246 Thr Val Phe Leu Phe Gly Leu Leu Ser Phe Ser Arg Ser Val Ala Leu
247                               420                               425                               430
248 Phe Arg Gly Tyr His Gly Pro Leu Asp Leu Tyr Pro Glu Phe Tyr Arg
249                               435                               440                               445
250 Ile Ala Thr Asp Pro Thr Ile His Thr Val Pro Glu Gly Arg Pro Val
251                               450                               455                               460
252 Asn Val Cys Val Gly Lys Glu Trp Tyr Arg Phe Pro Ser Ser Phe Leu
253 465                               470                               475                               480
254 Leu Pro Asp Asn Trp Gln Leu Gln Phe Ile Pro Ser Glu Phe Arg Gly
255                               485                               490                               495
256 Gln Leu Pro Lys Pro Phe Ala Glu Gly Pro Leu Ala Thr Arg Ile Val
257                               500                               505                               510
258 Pro Thr Asp Met Asn Asp Gln Asn Leu Glu Glu Pro Ser Arg Tyr Ile
259                               515                               520                               525
260 Asp Ile Ser Lys Cys His Tyr Leu Val Asp Leu Asp Thr Met Arg Glu
261                               530                               535                               540
262 Thr Pro Arg Glu Pro Lys Tyr Ser Ser Asn Lys Glu Glu Trp Ile Ser
263 545                               550                               555                               560
264 Leu Ala Tyr Arg Pro Phe Leu Asp Ala Ser Arg Ser Ser Lys Leu Leu
265                               565                               570                               575
266 Arg Ala Phe Tyr Val Pro Phe Leu Ser Asp Gln Tyr Thr Val Tyr Val
267                               580                               585                               590
268 Asn Tyr Thr Ile Leu Lys Pro Arg Lys Ala Lys Gln Ile Arg Lys Lys
269                               595                               600                               605
270 Ser Gly Gly
271                               610
274 <210> SEQ ID NO: 3
275 <211> LENGTH: 880
276 <212> TYPE: DNA
277 <213> ORGANISM: Homo sapiens
279 <220> FEATURE:
280 <221> NAME/KEY: CDS
281 <222> LOCATION: (113)...(877)
283 <400> SEQUENCE: 3
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285 agtgggttcaa ggttacaata agctgtgatc gtgccactgc attctacctg gg atg aca 118
286                                     Met Thr
287                                     1
289 gag tgg gac cct gtg cca cag agt gag acc ctg tct caa aaa aaa aaa 166
290 Glu Trp Asp Pro Val Pro Gln Ser Glu Thr Leu Ser Gln Lys Lys Lys
291                               5                               10                               15
293 cta tgt aaa tcc aag gag acg act tca cct gta ttg tac ctc tcc aag 214
294 Leu Cys Lys Ser Lys Glu Thr Thr Ser Pro Val Leu Tyr Leu Ser Lys
295                               20                               25                               30
297 ttc tgg aaa gtc gat gga ggg ttt act cag aac ttc aat cta tcc aga 262
298 Phe Trp Lys Val Asp Gly Gly Phe Thr Gln Asn Phe Asn Leu Ser Arg
299 35                               40                               45                               50

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VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date